

## **REMARKS**

### **Pending Claims**

Claims 1 and 50-74 are pending. Claims 62-74 are withdrawn pending rejoinder.

### **Restriction and Linking Claims**

Applicants assert the elected product group and new product claim 1 is properly linked to claims that recite a method of using the product of claim 1, as well as to claims drawn to combinations/subcombinations that require all the limitations of the claimed product of claim 1. The claimed malt (malted kernels or grain) and wort (mashed malted grain) are each part of the plant or portion of claim 1. The claimed beverages are products produced using the claimed plant or plant portion of claim 1. Accordingly, the malt, wort, and beverage claims, each requiring all the limitations of claim 1, are linked to claim 1 as products produced from the claimed plant and/or as combinations and/or subcombinations permitted by MPEP section 809. Allowance of the product claims 1 and 50-59 and rejoinder of the linked claims 62-74 is respectfully requested.

### **Examiner Interviews**

The Applicant's representative thanks Examiner Ibrahim for her kind assistance during the recent telephone interviews. The attached documents are copies of those submitted for discussion with the Examiner, and include, draft claims, sequence alignments, and listing of support in the specification for the claims. These documents are submitted for the prosecution record in this case, as requested by the Examiner.

### **Conclusion**

In light of the forgoing Amendment and Remarks, Applicant's respectfully assert the claims are in condition for allowance. Early notice of such allowance is solicited.

The Examiner is invited to telephone the undersigned attorney for clarification of any of these remarks and/or to otherwise speed prosecution of this case.



Respectfully submitted,

MERCHANT & GOULD P.C.  
P.O. Box 2903  
Minneapolis, Minnesota 55402-0903  
(612) 332-5300

Dated: 18 October 2007

By /Denise M. Kettelberger /  
Denise M. Kettelberger  
Reg. No. 33,924

Attachments: Fax cover sheet 09/07/07

# MEMORY TRANSMISSION REPORT

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## Merchant & Gould

An Intellectual Property Law Firm

3200 IDS Center  
80 South Eighth Street  
Minneapolis, Minnesota  
55402-2215 USA  
TEL 612.332.5300  
FAX 612.332.9081  
www.merchant-gould.com

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To: Examiner Ibrahim  
Company: USPTO  
Your Ref: 10/800,200  
Fax No.: 571-273-0797  
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From: D. Kettelberger  
Our Ref.: 12845.94540  
Fax No.: 612.332.9081  
Phone No.: 612-371-5268  
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### Document Transmitted:

#### Message:

Draft Claims, + Seq. Align attached for review + discussion.

Symone Kieft  
on behalf of D. Kettelberger

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M&G 12845.9USWO  
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**SEQUENCES:**

1. The specification and claims recite four LOX-1 proteins of interest, wild-type (cv Barke and cv Neruda) and Mutants D112 and A618. Please note that the WT nucleic acid sequences (SEQ ID NO: 1 and 5) and amino acid sequences (SEQ ID NO: 3 and 7) of LOX-1 are identical between these two barley varieties. (see the sequence comparison (1)).
2. Two mutants are exemplified, each containing a single nucleic acid change. In mutant A618, the gene is mutated at position 2311 changing G to A (SEQ ID NO: 6). See the nucleic acid comparison (2) at page 5. In mutant D112, nucleic acid 3574 is changed from G to A (SEQ ID NO: 2). See the nucleic acid comparison at page 7.
3. The point mutation in the nucleic acid sequence causes a splice variant mutant protein in mutant A618 (SEQ ID NO: 8), truncating the LOX-1 protein sequence at amino acid 378 and retaining a few non LOX-1 amino acids. See the amino acid comparison (3) on the first page. For mutant D112, the point mutation creates a stop codon, resulting in truncation of the LOX-1 protein at amino acid 665 (SEQ ID NO: 4). See the amino acid comparison at page 2.
4. Thus the two barley lox-1 wild type nucleic acid sequences are identical; the two mutant nucleic acid sequences each differ from the WT only in one amino acid. The two barley LOX-1 wild type protein sequences are identical; one mutant LOX-1 sequence, A618, is truncated at **378** and contains 21 additional non-LOX-1 amino acids; the second mutant, D112 is truncated at amino acid **665**.
5. The LOX-1 protein contains a LOX-1 enzymatic domain corresponding to amino acids **520-862**.

Barley	Lox-1 Gene	LOX-1 Protein	LOX-1 AA
WT cv Barke	SEQ ID NO: 1	SEQ ID NO: 3	1-862
WT cv Neruda	SEQ ID NO: 5	SEQ ID NO: 7	1-862
Mut D112	SEQ ID NO: 2	SEQ ID NO: 4	1-665
Mut A618	SEQ ID NO: 6	SEQ ID NO: 8	1-378 + 21 non

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## CLAIMS

1. In the proposed claim amendment, Claim 1 is amended to include the amino acids of the C-terminal enzymatic domain **520-862**, as you suggested. The WT barley sequence is identified as SEQ ID NO: **3** or **7**. (Note the two barley sequences are identical, and reference to only one would suffice.) Support for this amendment is found, for example at page 26, beginning at line 12:

The term LOX-1 protein is meant to cover the full length LOX-1 protein of barley as set forth in [SEQ ID NO: **3**] or [SEQ ID NO: **7**] or a functional homologue thereof. The active site of LOX-1 is situated in the C-terminal part of LOX-1. In particular is the region spanning amino acid residues 520-862 or parts thereof relevant for LOX-1 activity. Accordingly, in one embodiment null-LOX-1 barley preferably comprises a gene encoding a mutant form of LOX-1 **lacking some or all of amino acids 520-862** of LOX-1. Said mutant LOX-1 may also lack other amino acid residues which are present in wild-type LOX-1.

2. New claim 50 recites truncation of LOX-1 at a position at or between amino acids **378 and 665**. The mutants demonstrated in the examples contain a LOX-1 protein truncated at position **665** (D112 in Example 10) and at position **378** (A618 in Example 11). Example 10 describes the truncated D112 LOX-1 protein as:

The stop-codon in the LOX-1 encoding gene of the mutant D112 is predicted to result in a C-terminal truncation of 197 amino acids of the corresponding protein.... the sequence of which is listed in [SEQ ID NO:4].

Subtracting the 197 aa truncation from the 892 aa of the LOX-1 protein results in a mutant protein of containing amino acids **1-665** of LOX-1. See also Figure 15, listing mutant D112 as having 665 amino acids; see also SEQ ID NO:4 having 665 amino acids.

Example 11 describes the mutation in A618 to be in the intron 3 donor site, and causing a splice error in intron 3 leading to a stop codon in the intron 3 after translation of 399 amino acids. The truncated translated protein (SEQ ID NO: 8) includes both LOX-1 amino acids and amino acids of the intron. Comparison of the mutated protein and wild type LOX-1 demonstrates that the mutant protein includes amino acids **1-378** plus 21 non-LOX 1 amino acids. ( $378 + 21 = 399$ ).

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The specification further supports the truncation between 378 and 665. See, for example, page 30:

In one embodiment of the invention the barley plant comprises a gene encoding a mutant LOX-1, wherein said gene has a mutation in a splice site leading to mRNA encoding a protein consisting of amino acids **1 to 378** of [SEQ ID NO: 3] as well as an additional amino acid sequence not derived from LOX-1. Preferably, said mutant LOX-1 consists of the sequence as outlined in [SEQ ID NO: 8].

3. Proposed claim 51 recites amino acids **1-378**; Proposed claim 52 recites SEQ ID NO: **4** (D112) or **8** (A618). Each of these claims is supported by the specification, for example, as described above.
4. Proposed claims 53 -55 are amended to recite mutations of the gene in terms of the mutated protein, as you requested. Support for the gene mutations is found, for example in Figure 15 and in Examples 10 and 11. Mutant A618 contains a nucleic acid point mutation at position **2311** and mutant D112 contains a point mutation at position **3574**. Each point mutation results in a stop codon and truncated LOX-1 protein. The mutated genes have the sequences of SEQ ID NOs: **2** (D112) and **6** (A618)
5. Proposed claim 56 recites the ATCC deposit numbers for the mutant plants. Support is found, for example at page 30, including progeny.
6. Proposed claims 57 and 58 recite plant portions as kernels and embryos. Support for these plant portions is found, for example, at page 63 and particularly in the Examples demonstrating use of barley kernels for preparing malt, wort, and beer.
7. Proposed claim 58 recites a test for screening mutant LOX-1 activity in the M3 or M4 generation plants. Support is found in Examples 1, 2, 3, and 17, for example.
8. Proposed claims 60 and 61 are method of screening claims that have been restricted (original claim 48 for example). These claim should be marked (New and Withdrawn).
9. Proposed claims 62-64 are restricted claims that are withdrawn and subject to rejoinder on indication of allowable subject matter.

**What is claimed is:**

1. (Amended) A barley plant, ~~or a part thereof,~~ or a portion of said plant, comprising  
less than 5% of the LOX-1 activity of a wild-type barley plant  
a mutated LOX-1 protein lacking all or a portion of the C-terminal LOX-1  
enzymatic domain corresponding to amino acids 520 to 862 of wild type barley  
LOX-1 (SEQ ID NO: 3 or 7), wherein said plant exhibits null LOX-1 activity.
- 2-49. (Cancelled)
50. (New) The barley plant or portion according to claim 1, wherein said mutated LOX-1 protein is truncated at or between amino acids 378 and 665 of wild-type barley LOX-1.
51. (New) The barley plant or portion according to claim 1, wherein said mutated LOX-1 protein consists essentially of amino acids 1-378 of wild-type barley LOX-1 (SEQ ID NO: 3 or 7).
52. (New) The barley plant or portion according to claim 1, wherein said mutated LOX-1 protein has the amino acid sequence of SEQ ID NO. 4 or 8.
53. (New) The barley plant or portion according to claim 1, wherein said mutated LOX-1 protein is encoded by a gene that comprises a premature stop codon at or between nucleotides 2311 and 3574 of wild-type genomic barley lox-1 (SEQ ID NO: 1 or 5).
54. (New) The barley plant or portion according to claim 1, wherein said mutated LOX-1 protein is encoded by a gene that comprises a stop codon at nucleotides 3572-3574 of wild-type genomic barley lox-1 (SEQ ID NO: 1 or 5).
55. (New) The barley plant or portion according to claim 1, wherein said mutated LOX-1 protein is encoded by a gene that comprises the nucleic acid sequence of SEQ ID NO: 2 or 6.
56. (New) The barley plant or portion according to claim 1, wherein said plant has ATCC accession No. PTA-5847 or PTA-5584, or is a progeny plant thereof.
57. (New) The barley plant or portion according to claim 1, wherein said portion comprises a kernel.
58. (New) The barley plant or portion according to claim 1, wherein said portion comprises an embryo.
59. (New) The barley plant or portion according to claim 1, wherein said LOX-1 activity is determined in homogenized embryo tissue of M3 or M4 plant kernels.

60. (New and **Withdrawn**) A method for selecting mutant barley plants having null LOX-1 activity, comprising:
- a. breeding mutagenized barley plants or tissue obtained therefrom to produce generation Mx barley plants, where x is at least 2; and
  - b. selecting plants having null LOX-1 activity in kernel tissue of said generation Mx plants.
61. (New and **Withdrawn**) The method of claim 60, wherein said selecting is of generation M3 or M4 plants.
62. (New and Withdrawn) A **malt** composition comprising malted kernels of the plant of claim 1.
63. (New and Withdrawn) A **malt** composition comprising malted kernels of the plant of claim 54.
64. (New and Withdrawn) A **wort** composition comprising malted and mashed kernels of a plant of claim 1.
65. (New and Withdrawn) A **beverage** prepared from the plant or plant portion of claim 1, wherein the plant or portion is malted or unmalted.
66. (New and Withdrawn) A **beverage** prepared from the plant or plant portion of claim 54, wherein the plant or portion is malted or unmalted.
67. (New and Withdrawn) A **beverage** prepared from the plant or plant portion of claim 1, wherein the beverage is non-fermented or fermented.
68. (New and Withdrawn) A **beverage** prepared from the plant or plant portion of claim 1, wherein the beverage contains 9, 12, 13-trihydroxyoctadecanoic acid and 9, 10, 13-trihydroxyoctadecanoic acid in a ratio of no more than 1.8.
69. (New and Withdrawn) **Beer** prepared from the plant or plant portion of claim 1.
70. (New and Withdrawn) **Beer** prepared from the plant or plant portion of claim 54.
71. (New and Withdrawn) **Beer** prepared from kernels of the plant of claim 1.
72. (New and Withdrawn) **Beer** prepared from grain of the plant of claim 1.
73. (New and Withdrawn) **Beer** prepared from malted grain of the plant of claim 1.
74. (New and Withdrawn) **Beer** prepared from mashed malted grain of the plant of claim 1.



CLUSTAL W (1.8) multiple sequence alignment

LOI-1

Compare WT cv Barke vs Neruda  
- identical -

WT  
WT

SEQID3 Barke  
SEQID7 Neruda

MLLGGLIDTLTGANKSARLKGTVVLMRKNVLDLNDFGATIIDGIGEFGLGKGVTCQLISST  
MLLGGLIDTLTGANKSARLKGTVVLMRKNVLDLNDFGATIIDGIGEFGLGKGVTCQLISST  
\*\*\*\*\*

SEQID3  
SEQID7  
AVDQDNGGRGKVGAEAELEQWVTSPLSTTGESKFGLTFDWEVEKLGVPGAIVVNNYHSS  
AVDQDNGGRGKVGAEAELEQWVTSPLSTTGESKFGLTFDWEVEKLGVPGAIVVNNYHSS  
\*\*\*\*\*

SEQID3  
SEQID7  
EFLKKTITLHDVPGRSGNLTFFVANSWIYPAANYRYSRVFFANDTYLPSQMPAALKPYRDD  
EFLKKTITLHDVPGRSGNLTFFVANSWIYPAANYRYSRVFFANDTYLPSQMPAALKPYRDD  
\*\*\*\*\*

SEQID3  
SEQID7  
ELRNLRGDDQQGPYQEHDRIYRYDVYNDLGEGRPILGGNSDHPYPRRGRTERKPNASDPS  
ELRNLRGDDQQGPYQEHDRIYRYDVYNDLGEGRPILGGNSDHPYPRRGRTERKPNASDPS  
\*\*\*\*\*

SEQID3  
SEQID7  
LESRLSLEQIYVPRDEKFGHLKTSDFLGYSIKAITQGILPAVRTYVDTPGGEFDSFQDI  
LESRLSLEQIYVPRDEKFGHLKTSDFLGYSIKAITQGILPAVRTYVDTPGGEFDSFQDI  
\*\*\*\*\*

SEQID3  
SEQID7  
INLYEGGIKLPKVAALEELRKQFPLQLIKDLLPVGGDSLLKLPVPHIIQENKQAWRTDEE  
INLYEGGIKLPKVAALEELRKQFPLQLIKDLLPVGGDSLLKLPVPHIIQENKQAWRTDEE  
\*\*\*\*\*

SEQID3  
SEQID7  
FAREVLAGVNPVMITRLTEFPKSSLDPSKFGDHTSTITAHEIEKNLEGLTVQQALESNR  
FAREVLAGVNPVMITRLTEFPKSSLDPSKFGDHTSTITAHEIEKNLEGLTVQQALESNR  
\*\*\*\*\*

SEQID3  
SEQID7  
LYILDHHRFMPFLIDVNNLPGNFIYATRITLFFLRGDGRLTPLAIELSEPIIQGGLTTAK  
LYILDHHRFMPFLIDVNNLPGNFIYATRITLFFLRGDGRLTPLAIELSEPIIQGGLTTAK  
\*\*\*\*\*

SEQID3  
SEQID7  
SKVYTPVPSGSVEGWVWELAKAYVAVNDSGWHQLVSHWLNTHAVMEPFVISTNRHLSVTH  
SKVYTPVPSGSVEGWVWELAKAYVAVNDSGWHQLVSHWLNTHAVMEPFVISTNRHLSVTH  
\*\*\*\*\*

SEQID3  
SEQID7  
PVHKLLSPHYRDTMTINALARQTLINAGGIFEMTVFPGKFALGMSAVVYKDWKFTEQGLP  
PVHKLLSPHYRDTMTINALARQTLINAGGIFEMTVFPGKFALGMSAVVYKDWKFTEQGLP  
\*\*\*\*\*

SEQID3  
SEQID7  
DDLKRGMAVEDPSSPYKVRLLVSDYPYAADGLAIWHAIEQYVSEYLAIYYPNDGVLQGD  
DDLKRGMAVEDPSSPYKVRLLVSDYPYAADGLAIWHAIEQYVSEYLAIYYPNDGVLQGD  
\*\*\*\*\*

SEQID3  
SEQID7  
TEVQAWWKETREVGHGDLKDAPWWPKMQSVPELAKACTTIIWIGSALHAAVNFGQYPYAG  
TEVQAWWKETREVGHGDLKDAPWWPKMQSVPELAKACTTIIWIGSALHAAVNFGQYPYAG  
\*\*\*\*\*

SEQID3  
SEQID7  
FLPNRPTVSRRRMPEPGTEEYAELEDPERAFIHTITSQIQTIIGVSLLEVL SKHSSDEL  
FLPNRPTVSRRRMPEPGTEEYAELEDPERAFIHTITSQIQTIIGVSLLEVL SKHSSDEL  
\*\*\*\*\*

SEQID3  
SEQID7  
YLGQRDTPEWTSDPKALEVFKRFSRDLVEIESKVVG MNHDP ELK NRNGPAKF PYMLLYPN  
YLGQRDTPEWTSDPKALEVFKRFSRDLVEIESKVVG MNHDP ELK NRNGPAKF PYMLLYPN  
\*\*\*\*\*

SEQID3  
SEQID7  
TSDHKGAAAGLTAKGIPNSISI  
TSDHKGAAAGLTAKGIPNSISI  
\*\*\*\*\*

①

LOX-1 NA

Compare v<sub>0</sub> (ID 5, 1)  
mutant (ID 6, 2)

2311 (P5)  
3574 (P7)

CLUSTAL W (1.8) multiple sequence alignment

EACH DIFFER 1 NA

63

WT  
MUT  
WT  
MUT

SEQID5 Neruda  
SEQID6 A618  
SEQID1 Barke  
SEQID2 D112

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ATGCTGCTGGGAGGGCTGATCGACACCCTCACGGGGGCGAACAAGAGCGCCCGGCTCAAG
ATGCTGCTGGGAGGGCTGATCGACACCCTCACGGGGGCGAACAAGAGCGCCCGGCTCAAG
ATGCTGCTGGGAGGGCTGATCGACACCCTCACGGGGGCGAACAAGAGCGCCCGGCTCAAG
ATGCTGCTGGGAGGGCTGATCGACACCCTCACGGGGGCGAACAAGAGCGCCCGGCTCAAG
*****

SEQID5      GGCACGGTGGTGCTCATGCGCAAGAACGTGCTGGACCTCAACGACTTCGGCGCCACCATC
SEQID6      GGCACGGTGGTGCTCATGCGCAAGAACGTGCTGGACCTCAACGACTTCGGCGCCACCATC
SEQID1      GGCACGGTGGTGCTCATGCGCAAGAACGTGCTGGACCTCAACGACTTCGGCGCCACCATC
SEQID2      GGCACGGTGGTGCTCATGCGCAAGAACGTGCTGGACCTCAACGACTTCGGCGCCACCATC
*****

SEQID5      ATCGACGGCATCGGCGAGTTCCTCGGCAAGGGCGTCACCTGCCAGCTTATCAGCTCCACC
SEQID6      ATCGACGGCATCGGCGAGTTCCTCGGCAAGGGCGTCACCTGCCAGCTTATCAGCTCCACC
SEQID1      ATCGACGGCATCGGCGAGTTCCTCGGCAAGGGCGTCACCTGCCAGCTTATCAGCTCCACC
SEQID2      ATCGACGGCATCGGCGAGTTCCTCGGCAAGGGCGTCACCTGCCAGCTTATCAGCTCCACC
*****

SEQID5      GCCGTCGACCAAGGTAATCACTACCCTCCTCCGGCCTTCTCCTCTGTTTACAAGATATAG
SEQID6      GCCGTCGACCAAGGTAATCACTACCCTCCTCCGGCCTTCTCCTCTGTTTACAAGATATAG
SEQID1      GCCGTCGACCAAGGTAATCACTACCCTCCTCCGGCCTTCTCCTCTGTTTACAAGATATAG
SEQID2      GCCGTCGACCAAGGTAATCACTACCCTCCTCCGGCCTTCTCCTCTGTTTACAAGATATAG
*****

SEQID5      TATTTCTTTTCGTGTGGGCCGGCGGCCATGGATGGATGGATGTGTCTGGATCGGCTAAAGA
SEQID6      TATTTCTTTTCGTGTGGGCCGGCGGCCATGGATGGATGGATGTGTCTGGATCGGCTAAAGA
SEQID1      TATTTCTTTTCGTGTGGGCCGGCGGCCATGGATGGATGGATGTGTCTGGATCGGCTAAAGA
SEQID2      TATTTCTTTTCGTGTGGGCCGGCGGCCATGGATGGATGGATGTGTCTGGATCGGCTAAAGA
*****

SEQID5      AGATAGGATAGCTAGCCCTGGCCGGTCGTCTTTACCTGAGCATGGGCATATGCCATCGAA
SEQID6      AGATAGGATAGCTAGCCCTGGCCGGTCGTCTTTACCTGAGCATGGGCATATGCCATCGAA
SEQID1      AGATAGGATAGCTAGCCCTGGCCGGTCGTCTTTACCTGAGCATGGGCATATGCCATCGAA
SEQID2      AGATAGGATAGCTAGCCCTGGCCGGTCGTCTTTACCTGAGCATGGGCATATGCCATCGAA
*****

SEQID5      AAAAGAGACAACAGCATGCATGCATGGTGCGCGCACCAGACCACGCAGAGCACC GGATGC
SEQID6      AAAAGAGACAACAGCATGCATGCATGGTGCGCGCACCAGACCACGCAGAGCACC GGATGC
SEQID1      AAAAGAGACAACAGCATGCATGCATGGTGCGCGCACCAGACCACGCAGAGCACC GGATGC
SEQID2      AAAAGAGACAACAGCATGCATGCATGGTGCGCGCACCAGACCACGCAGAGCACC GGATGC
*****

SEQID5      TCGAGACAAAGCAACACAACAAGCAAGGACGACACGTCAAAAGCAACACAACAAGCAAGG
SEQID6      TCGAGACAAAGCAACACAACAAGCAAGGACGACACGTCAAAAGCAACACAACAAGCAAGG
SEQID1      TCGAGACAAAGCAACACAACAAGCAAGGACGACACGTCAAAAGCAACACAACAAGCAAGG
SEQID2      TCGAGACAAAGCAACACAACAAGCAAGGACGACACGTCAAAAGCAACACAACAAGCAAGG
*****

SEQID5      ACGGCACGTCAAAAGCAACACAACCTAAACTAAAGCACAAAGACGTAAGAGCAAGCACA
SEQID6      ACGGCACGTCAAAAGCAACACAACCTAAACTAAAGCACAAAGACGTAAGAGCAAGCACA
SEQID1      ACGGCACGTCAAAAGCAACACAACCTAAACTAAAGCACAAAGACGTAAGAGCAAGCACA
SEQID2      ACGGCACGTCAAAAGCAACACAACCTAAACTAAAGCACAAAGACGTAAGAGCAAGCACA
*****

```

540

2

SEQID5	CAATCAGCAGGCTATAAACAGTTGTCATCAAAAACAACGCTGGAAGAGAGAGAGAAGGAA
SEQID6	CAATCAGCAGGCTATAAACAGTTGTCATCAAAAACAACGCTGGAAGAGAGAGAGAAGGAA
SEQID1	CAATCAGCAGGCTATAAACAGTTGTCATCAAAAACAACGCTGGAAGAGAGAGAGAAGGAA
SEQID2	CAATCAGCAGGCTATAAACAGTTGTCATCAAAAACAACGCTGGAAGAGAGAGAGAAGGAA
	*****
SEQID5	GGAAGTAGTAGCCATGAAAAATTAAATCACCGGGCGTTGCTCTTTGCCCAACAATTAATC
SEQID6	GGAAGTAGTAGCCATGAAAAATTAAATCACCGGGCGTTGCTCTTTGCCCAACAATTAATC
SEQID1	GGAAGTAGTAGCCATGAAAAATTAAATCACCGGGCGTTGCTCTTTGCCCAACAATTAATC
SEQID2	GGAAGTAGTAGCCATGAAAAATTAAATCACCGGGCGTTGCTCTTTGCCCAACAATTAATC
	*****
SEQID5	AAGCAGGATACGTGGCATGTATAGTTCTTGTAAGTAACTAAGCATGTGATATGAGAAGG
SEQID6	AAGCAGGATACGTGGCATGTATAGTTCTTGTAAGTAACTAAGCATGTGATATGAGAAGG
SEQID1	AAGCAGGATACGTGGCATGTATAGTTCTTGTAAGTAACTAAGCATGTGATATGAGAAGG
SEQID2	AAGCAGGATACGTGGCATGTATAGTTCTTGTAAGTAACTAAGCATGTGATATGAGAAGG
	*****
SEQID5	TACGTGGTGGTGCAGACAACGGCGGTTCGCGGGAAGGTGGGCGCGGAGGCGGAGCTGGAGC
SEQID6	TACGTGGTGGTGCAGACAACGGCGGTTCGCGGGAAGGTGGGCGCGGAGGCGGAGCTGGAGC
SEQID1	TACGTGGTGGTGCAGACAACGGCGGTTCGCGGGAAGGTGGGCGCGGAGGCGGAGCTGGAGC
SEQID2	TACGTGGTGGTGCAGACAACGGCGGTTCGCGGGAAGGTGGGCGCGGAGGCGGAGCTGGAGC
	*****
SEQID5	AGTGGGTGACGAGCCTGCCGTGCTGACGACGGGGGAGTCCAAGTTCGGCCTCACCTTCG
SEQID6	AGTGGGTGACGAGCCTGCCGTGCTGACGACGGGGGAGTCCAAGTTCGGCCTCACCTTCG
SEQID1	AGTGGGTGACGAGCCTGCCGTGCTGACGACGGGGGAGTCCAAGTTCGGCCTCACCTTCG
SEQID2	AGTGGGTGACGAGCCTGCCGTGCTGACGACGGGGGAGTCCAAGTTCGGCCTCACCTTCG
	*****
SEQID5	ACTGGGAGGTGGAGAAGCTCGGGGTGCCGGGCGCCATCGTCGTCAACAACCTACCACAGCT
SEQID6	ACTGGGAGGTGGAGAAGCTCGGGGTGCCGGGCGCCATCGTCGTCAACAACCTACCACAGCT
SEQID1	ACTGGGAGGTGGAGAAGCTCGGGGTGCCGGGCGCCATCGTCGTCAACAACCTACCACAGCT
SEQID2	ACTGGGAGGTGGAGAAGCTCGGGGTGCCGGGCGCCATCGTCGTCAACAACCTACCACAGCT
	*****
SEQID5	CCGAGTTCCTGCTTAAAACCATCACCTCCACGACGTCCCCGGCCGAGCGGCAACCTCA
SEQID6	CCGAGTTCCTGCTTAAAACCATCACCTCCACGACGTCCCCGGCCGAGCGGCAACCTCA
SEQID1	CCGAGTTCCTGCTTAAAACCATCACCTCCACGACGTCCCCGGCCGAGCGGCAACCTCA
SEQID2	CCGAGTTCCTGCTTAAAACCATCACCTCCACGACGTCCCCGGCCGAGCGGCAACCTCA
	*****
SEQID5	CCTTCGTGCGCAACTCATGGATCTACCCGCGCCCAACTACCGATACAGCCGCGTCTTCT
SEQID6	CCTTCGTGCGCAACTCATGGATCTACCCGCGCCCAACTACCGATACAGCCGCGTCTTCT
SEQID1	CCTTCGTGCGCAACTCATGGATCTACCCGCGCCCAACTACCGATACAGCCGCGTCTTCT
SEQID2	CCTTCGTGCGCAACTCATGGATCTACCCGCGCCCAACTACCGATACAGCCGCGTCTTCT
	*****
SEQID5	TCGCCAACGACGTGCGTGGATTTTCCTCTACTTTCCTCTCCTTTCATTTTCACCGCCTTC
SEQID6	TCGCCAACGACGTGCGTGGATTTTCCTCTACTTTCCTCTCCTTTCATTTTCACCGCCTTC
SEQID1	TCGCCAACGACGTGCGTGGATTTTCCTCTACTTTCCTCTCCTTTCATTTTCACCGCCTTC
SEQID2	TCGCCAACGACGTGCGTGGATTTTCCTCTACTTTCCTCTCCTTTCATTTTCACCGCCTTC
	*****

SEQID5	GTCATTTCATGGTCGATCATTAAGTCTTGCCAGGACAATAGATGATGAGCTAGGAGTGGTT
SEQID6	GTCATTTCATGGTCGATCATTAAGTCTTGCCAGGACAATAGATGATGAGCTAGGAGTGGTT
SEQID1	GTCATTTCATGGTCGATCATTAAGTCTTGCCAGGACAATAGATGATGAGCTAGGAGTGGTT
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SEQID5	CAGATCGACACAAGATTGAATGAAAGTTGCACCGTGGCACCCTGGCAGCGTGGTAGGTGA
SEQID6	CAGATCGACACAAGATTGAATGAAAGTTGCACCGTGGCACCCTGGCAGCGTGGTAGGTGA
SEQID1	CAGATCGACACAAGATTGAATGAAAGTTGCACCGTGGCACCCTGGCAGCGTGGTAGGTGA
SEQID2	CAGATCGACACAAGATTGAATGAAAGTTGCACCGTGGCACCCTGGCAGCGTGGTAGGTGA
	*****
SEQID5	AAATAACTGTTGCACGGATCCACCCACATGATTGTTTTTCATGAATAAACTTTTAAAGGAT
SEQID6	AAATAACTGTTGCACGGATCCACCCACATGATTGTTTTTCATGAATAAACTTTTAAAGGAT
SEQID1	AAATAACTGTTGCACGGATCCACCCACATGATTGTTTTTCATGAATAAACTTTTAAAGGAT
SEQID2	AAATAACTGTTGCACGGATCCACCCACATGATTGTTTTTCATGAATAAACTTTTAAAGGAT
	*****
SEQID5	GTGTCTAGCCACATCTAGATGCATGTCACATAATTATTGCATACCAAACGATTAAATTA
SEQID6	GTGTCTAGCCACATCTAGATGCATGTCACATAATTATTGCATACCAAACGATTAAATTA
SEQID1	GTGTCTAGCCACATCTAGATGCATGTCACATAATTATTGCATACCAAACGATTAAATTA
SEQID2	GTGTCTAGCCACATCTAGATGCATGTCACATAATTATTGCATACCAAACGATTAAATTA
	*****
SEQID5	AGCATAAAAAGAAAAGGAAAAAATACTCACATATCTCGACGTAAGATCAATGATATAGT
SEQID6	AGCATAAAAAGAAAAGGAAAAAATACTCACATATCTCGACGTAAGATCAATGATATAGT
SEQID1	AGCATAAAAAGAAAAGGAAAAAATACTCACATATCTCGACGTAAGATCAATGATATAGT
SEQID2	AGCATAAAAAGAAAAGGAAAAAATACTCACATATCTCGACGTAAGATCAATGATATAGT
	*****
SEQID5	ATTTAGATATGCAATATTTATCTTACATCTAAACCTTTCTTCATTCCTAAATATAAGACA
SEQID6	ATTTAGATATGCAATATTTATCTTACATCTAAACCTTTCTTCATTCCTAAATATAAGACA
SEQID1	ATTTAGATATGCAATATTTATCTTACATCTAAACCTTTCTTCATTCCTAAATATAAGACA
SEQID2	ATTTAGATATGCAATATTTATCTTACATCTAAACCTTTCTTCATTCCTAAATATAAGACA
	*****
SEQID5	TTTGTAAGATTTCACTATGGACAACATACGAAACAAAATCAGTGGATCTCTCTATGCATT
SEQID6	TTTGTAAGATTTCACTATGGACAACATACGAAACAAAATCAGTGGATCTCTCTATGCATT
SEQID1	TTTGTAAGATTTCACTATGGACAACATACGAAACAAAATCAGTGGATCTCTCTATGCATT
SEQID2	TTTGTAAGATTTCACTATGGACAACATACGAAACAAAATCAGTGGATCTCTCTATGCATT
	*****
SEQID5	CATTATGTAGTCTATAATAAAATCTTTAAAAGATCGTATATTTTGCAACGGAGGGAGTAA
SEQID6	CATTATGTAGTCTATAATAAAATCTTTAAAAGATCGTATATTTTGCAACGGAGGGAGTAA
SEQID1	CATTATGTAGTCTATAATAAAATCTTTAAAAGATCGTATATTTTGCAACGGAGGGAGTAA
SEQID2	CATTATGTAGTCTATAATAAAATCTTTAAAAGATCGTATATTTTGCAACGGAGGGAGTAA
	*****

SEQID5	AACATAACTTTTTTAATAGTAATGTTGCACGGCTCCACACTCGCAGACGTACCTGCCGAGC
SEQID6	AACATAACTTTTTTAATAGTAATGTTGCACGGCTCCACACTCGCAGACGTACCTGCCGAGC
SEQID1	AACATAACTTTTTTAATAGTAATGTTGCACGGCTCCACACTCGCAGACGTACCTGCCGAGC
SEQID2	AACATAACTTTTTTAATAGTAATGTTGCACGGCTCCACACTCGCAGACGTACCTGCCGAGC
	*****
SEQID5	CAGATGCCGGCGGCGCTGAAGCCGTACCGCGACGACGAGCTCCGGAACCTGCGTGCGGAC
SEQID6	CAGATGCCGGCGGCGCTGAAGCCGTACCGCGACGACGAGCTCCGGAACCTGCGTGCGGAC
SEQID1	CAGATGCCGGCGGCGCTGAAGCCGTACCGCGACGACGAGCTCCGGAACCTGCGTGCGGAC
SEQID2	CAGATGCCGGCGGCGCTGAAGCCGTACCGCGACGACGAGCTCCGGAACCTGCGTGCGGAC
	*****
SEQID5	GACCAGCAGGGCCCGTACCAGGAGCACGACCGCATCTACCGCTACGACGTCTACAACGAC
SEQID6	GACCAGCAGGGCCCGTACCAGGAGCACGACCGCATCTACCGCTACGACGTCTACAACGAC
SEQID1	GACCAGCAGGGCCCGTACCAGGAGCACGACCGCATCTACCGCTACGACGTCTACAACGAC
SEQID2	GACCAGCAGGGCCCGTACCAGGAGCACGACCGCATCTACCGCTACGACGTCTACAACGAC
	*****
SEQID5	CTCGGCGAGGGCCGCCCCATCCTCGGCGGCAACTCCGACCACCTTACCCGCGCCGCGGC
SEQID6	CTCGGCGAGGGCCGCCCCATCCTCGGCGGCAACTCCGACCACCTTACCCGCGCCGCGGC
SEQID1	CTCGGCGAGGGCCGCCCCATCCTCGGCGGCAACTCCGACCACCTTACCCGCGCCGCGGC
SEQID2	CTCGGCGAGGGCCGCCCCATCCTCGGCGGCAACTCCGACCACCTTACCCGCGCCGCGGC
	*****
SEQID5	CGCACGGAGCGCAAGCCCCAACGCCAGCGACCCGAGCCTGGAGAGCCGGCTGTGCTGCTG
SEQID6	CGCACGGAGCGCAAGCCCCAACGCCAGCGACCCGAGCCTGGAGAGCCGGCTGTGCTGCTG
SEQID1	CGCACGGAGCGCAAGCCCCAACGCCAGCGACCCGAGCCTGGAGAGCCGGCTGTGCTGCTG
SEQID2	CGCACGGAGCGCAAGCCCCAACGCCAGCGACCCGAGCCTGGAGAGCCGGCTGTGCTGCTG
	*****
SEQID5	GAGCAGATCTACGTGCCGCGGGACGAGAAGTTCGGCCACCTCAAGACGTCCGACTTCCTG
SEQID6	GAGCAGATCTACGTGCCGCGGGACGAGAAGTTCGGCCACCTCAAGACGTCCGACTTCCTG
SEQID1	GAGCAGATCTACGTGCCGCGGGACGAGAAGTTCGGCCACCTCAAGACGTCCGACTTCCTG
SEQID2	GAGCAGATCTACGTGCCGCGGGACGAGAAGTTCGGCCACCTCAAGACGTCCGACTTCCTG
	*****
SEQID5	GGCTACTCCATCAAGGCCATCACGCAGGGCATCCTGCCGGCCGTGCGCACCTACGTGGAC
SEQID6	GGCTACTCCATCAAGGCCATCACGCAGGGCATCCTGCCGGCCGTGCGCACCTACGTGGAC
SEQID1	GGCTACTCCATCAAGGCCATCACGCAGGGCATCCTGCCGGCCGTGCGCACCTACGTGGAC
SEQID2	GGCTACTCCATCAAGGCCATCACGCAGGGCATCCTGCCGGCCGTGCGCACCTACGTGGAC
	*****
SEQID5	ACCACCCCGGCGAGTTGCACTCCTTCCAGGACATCATCAACCTCTATGAGGGCGGCATC
SEQID6	ACCACCCCGGCGAGTTGCACTCCTTCCAGGACATCATCAACCTCTATGAGGGCGGCATC
SEQID1	ACCACCCCGGCGAGTTGCACTCCTTCCAGGACATCATCAACCTCTATGAGGGCGGCATC
SEQID2	ACCACCCCGGCGAGTTGCACTCCTTCCAGGACATCATCAACCTCTATGAGGGCGGCATC
	*****
SEQID5	AAGCTGCCCAAGGTGGCCGCCCTGGAGGAGCTCCGTAAGCAGTTCCCGCTCCAGCTCATC
SEQID6	AAGCTGCCCAAGGTGGCCGCCCTGGAGGAGCTCCGTAAGCAGTTCCCGCTCCAGCTCATC
SEQID1	AAGCTGCCCAAGGTGGCCGCCCTGGAGGAGCTCCGTAAGCAGTTCCCGCTCCAGCTCATC
SEQID2	AAGCTGCCCAAGGTGGCCGCCCTGGAGGAGCTCCGTAAGCAGTTCCCGCTCCAGCTCATC
	*****

2160

SEQID5 AAGGACCTCCTCCCCGTCGGCGGCGACTCCCTGCTTAAGCTCCCCGTGCCCCACATCATC 2220  
 SEQID6 AAGGACCTCCTCCCCGTCGGCGGCGACTCCCTGCTTAAGCTCCCCGTGCCCCACATCATC  
 SEQID1 AAGGACCTCCTCCCCGTCGGCGGCGACTCCCTGCTTAAGCTCCCCGTGCCCCACATCATC  
 SEQID2 AAGGACCTCCTCCCCGTCGGCGGCGACTCCCTGCTTAAGCTCCCCGTGCCCCACATCATC  
 \*\*\*\*\*

SEQID5 CAGGAGAACAAGCAGGCGTGGAGGACCGACGAGGAGTTCGCACGGGAGGTGCTCGCCGGC 2280  
 SEQID6 CAGGAGAACAAGCAGGCGTGGAGGACCGACGAGGAGTTCGCACGGGAGGTGCTCGCCGGC  
 SEQID1 CAGGAGAACAAGCAGGCGTGGAGGACCGACGAGGAGTTCGCACGGGAGGTGCTCGCCGGC  
 SEQID2 CAGGAGAACAAGCAGGCGTGGAGGACCGACGAGGAGTTCGCACGGGAGGTGCTCGCCGGC  
 \*\*\*\*\*

SEQID5 GTCAACCCGGTCATGATCACGCGTCTCACGGT<sup>23</sup> **2311** GTAGTCAGCGATTATTTGTTTCATTGTGTG  
 SEQID6 **A618** GTCAACCCGGTCATGATCACGCGTCTCACGATGAGTCAGCGATTATTTGTTTCATTGTGTG  
 SEQID1 GTCAACCCGGTCATGATCACGCGTCTCACGGTGTAGTCAGCGATTATTTGTTTCATTGTGTG  
 SEQID2 GTCAACCCGGTCATGATCACGCGTCTCACGGTGTAGTCAGCGATTATTTGTTTCATTGTGTG  
 \*\*\*\*\*

SEQID5 TGTATGGTGTCCATGGTGAGAAAGTGCAGATCTTGATTGCGTTGGGTGCGATGCACGCA  
 SEQID6 TGTATGGTGTCCATGGTGAGAAAGTGCAGATCTTGATTGCGTTGGGTGCGATGCACGCA  
 SEQID1 TGTATGGTGTCCATGGTGAGAAAGTGCAGATCTTGATTGCGTTGGGTGCGATGCACGCA  
 SEQID2 TGTATGGTGTCCATGGTGAGAAAGTGCAGATCTTGATTGCGTTGGGTGCGATGCACGCA  
 \*\*\*\*\*

SEQID5 TGCTGCATGCATGCAGGAGTTCCCGCCAAAAAGTAGTCTGGACCCTAGCAAGTTTGGTGA  
 SEQID6 TGCTGCATGCATGCAGGAGTTCCCGCCAAAAAGTAGTCTGGACCCTAGCAAGTTTGGTGA  
 SEQID1 TGCTGCATGCATGCAGGAGTTCCCGCCAAAAAGTAGTCTGGACCCTAGCAAGTTTGGTGA  
 SEQID2 TGCTGCATGCATGCAGGAGTTCCCGCCAAAAAGTAGTCTGGACCCTAGCAAGTTTGGTGA  
 \*\*\*\*\*

SEQID5 CCACACCAGCACCATCACGGCGGAGCACATAGAGAAGAACCTCGAGGGCCTCACGGTGCA  
 SEQID6 CCACACCAGCACCATCACGGCGGAGCACATAGAGAAGAACCTCGAGGGCCTCACGGTGCA  
 SEQID1 CCACACCAGCACCATCACGGCGGAGCACATAGAGAAGAACCTCGAGGGCCTCACGGTGCA  
 SEQID2 CCACACCAGCACCATCACGGCGGAGCACATAGAGAAGAACCTCGAGGGCCTCACGGTGCA  
 \*\*\*\*\*

SEQID5 GCAGGTAATTGGTCCAAGCCATCGACATCAACTATGATTTACCTAGGAGTAATTGGTAGC  
 SEQID6 GCAGGTAATTGGTCCAAGCCATCGACATCAACTATGATTTACCTAGGAGTAATTGGTAGC  
 SEQID1 GCAGGTAATTGGTCCAAGCCATCGACATCAACTATGATTTACCTAGGAGTAATTGGTAGC  
 SEQID2 GCAGGTAATTGGTCCAAGCCATCGACATCAACTATGATTTACCTAGGAGTAATTGGTAGC  
 \*\*\*\*\*

SEQID5 TGTAGATAATTTGGCTTCGTTGCAATTAATTTGATGCTGGCCGATCAAGTGATCGTATTG  
 SEQID6 TGTAGATAATTTGGCTTCGTTGCAATTAATTTGATGCTGGCCGATCAAGTGATCGTATTG  
 SEQID1 TGTAGATAATTTGGCTTCGTTGCAATTAATTTGATGCTGGCCGATCAAGTGATCGTATTG  
 SEQID2 TGTAGATAATTTGGCTTCGTTGCAATTAATTTGATGCTGGCCGATCAAGTGATCGTATTG  
 \*\*\*\*\*

SEQID5 GGTTTGAAATTTGCAGGCGCTGGAAAGCAACAGGCTGTACATCCTTGATCACCATGACCG  
 SEQID6 GGTTTGAAATTTGCAGGCGCTGGAAAGCAACAGGCTGTACATCCTTGATCACCATGACCG  
 SEQID1 GGTTTGAAATTTGCAGGCGCTGGAAAGCAACAGGCTGTACATCCTTGATCACCATGACCG  
 SEQID2 GGTTTGAAATTTGCAGGCGCTGGAAAGCAACAGGCTGTACATCCTTGATCACCATGACCG  
 \*\*\*\*\*

SEQID5 GTTCATGCCGTTCCCTGATCGACGTCAACAACCTGCCCGGCAACTTCATCTACGCCACGAG  
 SEQID6 GTTCATGCCGTTCCCTGATCGACGTCAACAACCTGCCCGGCAACTTCATCTACGCCACGAG  
 SEQID1 GTTCATGCCGTTCCCTGATCGACGTCAACAACCTGCCCGGCAACTTCATCTACGCCACGAG  
 SEQID2 GTTCATGCCGTTCCCTGATCGACGTCAACAACCTGCCCGGCAACTTCATCTACGCCACGAG  
 \*\*\*\*\*

SEQID5 GACCCCTCTTCTTCTGCGCGGCGACGGCAGGCTCACGCCGCTCGCCATCGAGCTGAGCGA  
 SEQID6 GACCCCTCTTCTTCTGCGCGGCGACGGCAGGCTCACGCCGCTCGCCATCGAGCTGAGCGA  
 SEQID1 GACCCCTCTTCTTCTGCGCGGCGACGGCAGGCTCACGCCGCTCGCCATCGAGCTGAGCGA  
 SEQID2 GACCCCTCTTCTTCTGCGCGGCGACGGCAGGCTCACGCCGCTCGCCATCGAGCTGAGCGA  
 \*\*\*\*\*

SEQID5 GCCCATCATCCAGGGCGGCCTTACCACGGCCAAGAGCAAGGTTTACACGCCGGTGCCAG  
 SEQID6 GCCCATCATCCAGGGCGGCCTTACCACGGCCAAGAGCAAGGTTTACACGCCGGTGCCAG  
 SEQID1 GCCCATCATCCAGGGCGGCCTTACCACGGCCAAGAGCAAGGTTTACACGCCGGTGCCAG  
 SEQID2 GCCCATCATCCAGGGCGGCCTTACCACGGCCAAGAGCAAGGTTTACACGCCGGTGCCAG  
 \*\*\*\*\*

SEQID5 CGGCTCCGTCTGAAGGCTGGGTGTGGGAGCTCGCCAAGGCCTACGTGCGCGTCAATGACTC  
 SEQID6 CGGCTCCGTCTGAAGGCTGGGTGTGGGAGCTCGCCAAGGCCTACGTGCGCGTCAATGACTC  
 SEQID1 CGGCTCCGTCTGAAGGCTGGGTGTGGGAGCTCGCCAAGGCCTACGTGCGCGTCAATGACTC  
 SEQID2 CGGCTCCGTCTGAAGGCTGGGTGTGGGAGCTCGCCAAGGCCTACGTGCGCGTCAATGACTC  
 \*\*\*\*\*

SEQID5 CGGGTGGCACCAGCTCGTCAGCCACTGGTACGTTCTCCACGGTCGATGTGATTCACTCAG  
 SEQID6 CGGGTGGCACCAGCTCGTCAGCCACTGGTACGTTCTCCACGGTCGATGTGATTCACTCAG  
 SEQID1 CGGGTGGCACCAGCTCGTCAGCCACTGGTACGTTCTCCACGGTCGATGTGATTCACTCAG  
 SEQID2 CGGGTGGCACCAGCTCGTCAGCCACTGGTACGTTCTCCACGGTCGATGTGATTCACTCAG  
 \*\*\*\*\*

SEQID5 TCGATGCACAACAACCTGATCGAAATATGATTGATTGAAACGCGCAGGCTGAACACTCACG  
 SEQID6 TCGATGCACAACAACCTGATCGAAATATGATTGATTGAAACGCGCAGGCTGAACACTCACG  
 SEQID1 TCGATGCACAACAACCTGATCGAAATATGATTGATTGAAACGCGCAGGCTGAACACTCACG  
 SEQID2 TCGATGCACAACAACCTGATCGAAATATGATTGATTGAAACGCGCAGGCTGAACACTCACG  
 \*\*\*\*\*

SEQID5 CGGTGATGGAGCCGTTTCGTGATCTCGACGAACCGGCACCTTAGCGTGACGCACCCGGTGC  
 SEQID6 CGGTGATGGAGCCGTTTCGTGATCTCGACGAACCGGCACCTTAGCGTGACGCACCCGGTGC  
 SEQID1 CGGTGATGGAGCCGTTTCGTGATCTCGACGAACCGGCACCTTAGCGTGACGCACCCGGTGC  
 SEQID2 CGGTGATGGAGCCGTTTCGTGATCTCGACGAACCGGCACCTTAGCGTGACGCACCCGGTGC  
 \*\*\*\*\*

SEQID5 ACAAGCTGCTGAGCCCGCACTACCGCGACACCATGACCATCAACGCGCTGGCGCGGCAGA  
 SEQID6 ACAAGCTGCTGAGCCCGCACTACCGCGACACCATGACCATCAACGCGCTGGCGCGGCAGA  
 SEQID1 ACAAGCTGCTGAGCCCGCACTACCGCGACACCATGACCATCAACGCGCTGGCGCGGCAGA  
 SEQID2 ACAAGCTGCTGAGCCCGCACTACCGCGACACCATGACCATCAACGCGCTGGCGCGGCAGA  
 \*\*\*\*\*

SEQID5 CGCTCATCAACGCCGGCGGCATCTTCGAGATGACGGTGTTCGCCGGCAAGTTCGCGTTGG 3240  
 SEQID6 CGCTCATCAACGCCGGCGGCATCTTCGAGATGACGGTGTTCGCCGGCAAGTTCGCGTTGG  
 SEQID1 CGCTCATCAACGCCGGCGGCATCTTCGAGATGACGGTGTTCGCCGGCAAGTTCGCGTTGG  
 SEQID2 CGCTCATCAACGCCGGCGGCATCTTCGAGATGACGGTGTTCGCCGGCAAGTTCGCGTTGG  
 \*\*\*\*\*

SEQID5 GGATGTCGGCCGTGGTGTACAAGGACTGGAAGTTCACCGAGCAGGGACTGCCGGACGATC  
SEQID6 GGATGTCGGCCGTGGTGTACAAGGACTGGAAGTTCACCGAGCAGGGACTGCCGGACGATC  
SEQID1 GGATGTCGGCCGTGGTGTACAAGGACTGGAAGTTCACCGAGCAGGGACTGCCGGACGATC  
SEQID2 GGATGTCGGCCGTGGTGTACAAGGACTGGAAGTTCACCGAGCAGGGACTGCCGGACGATC  
\*\*\*\*\*

SEQID5 TCATCAAGAGGTACGTACCTGGTAAATGTTATGAATGTGTAAAAACAAATTGGGCGTCTCG  
SEQID6 TCATCAAGAGGTACGTACCTGGTAAATGTTATGAATGTGTAAAAACAAATTGGGCGTCTCG  
SEQID1 TCATCAAGAGGTACGTACCTGGTAAATGTTATGAATGTGTAAAAACAAATTGGGCGTCTCG  
SEQID2 TCATCAAGAGGTACGTACCTGGTAAATGTTATGAATGTGTAAAAACAAATTGGGCGTCTCG  
\*\*\*\*\*

SEQID5 CTCACTGACAGGAACGTGGTAAAAAATGCAGGGGCATGGCGGTGGAGGACCCGTCGAG  
SEQID6 CTCACTGACAGGAACGTGGTAAAAAATGCAGGGGCATGGCGGTGGAGGACCCGTCGAG  
SEQID1 CTCACTGACAGGAACGTGGTAAAAAATGCAGGGGCATGGCGGTGGAGGACCCGTCGAG  
SEQID2 CTCACTGACAGGAACGTGGTAAAAAATGCAGGGGCATGGCGGTGGAGGACCCGTCGAG  
\*\*\*\*\*

SEQID5 CCCGTACAAGGTGCGGTTGCTGGTGTCTGGACTACCCGTACGCGGCGGACGGGCTGGCGAT  
SEQID6 CCCGTACAAGGTGCGGTTGCTGGTGTCTGGACTACCCGTACGCGGCGGACGGGCTGGCGAT  
SEQID1 CCCGTACAAGGTGCGGTTGCTGGTGTCTGGACTACCCGTACGCGGCGGACGGGCTGGCGAT  
SEQID2 CCCGTACAAGGTGCGGTTGCTGGTGTCTGGACTACCCGTACGCGGCGGACGGGCTGGCGAT  
\*\*\*\*\*

SEQID5 CTGGCAGCCATTGAGCAGTACGTGAGCGAGTACCTGGCCATCTACTACCCGAACGACGG  
SEQID6 CTGGCAGCCATTGAGCAGTACGTGAGCGAGTACCTGGCCATCTACTACCCGAACGACGG  
SEQID1 CTGGCAGCCATTGAGCAGTACGTGAGCGAGTACCTGGCCATCTACTACCCGAACGACGG  
SEQID2 CTGGCAGCCATTGAGCAGTACGTGAGCGAGTACCTGGCCATCTACTACCCGAACGACGG  
\*\*\*\*\*

SEQID5 CGTGCTGCAGGGCGATACGGAGGTGCAGGCGTGGTGAAGGAGACGCGGAGGTGCGGCA  
SEQID6 CGTGCTGCAGGGCGATACGGAGGTGCAGGCGTGGTGAAGGAGACGCGGAGGTGCGGCA  
SEQID1 CGTGCTGCAGGGCGATACGGAGGTGCAGGCGTGGTGAAGGAGACGCGGAGGTGCGGCA  
SEQID2 CGTGCTGCAGGGCGATACGGAGGTGCAGGCGTGGTGAAGGAGACGCGGAGGTGCGGCA  
\*\*\*\*\*

D112

3574

SEQID5 CGGCGACCTCAAGGACGCCCCATGGTGGCCCAAGATGCAAAGTGTGCCGGAGCTGGCCAA  
SEQID6 CGGCGACCTCAAGGACGCCCCATGGTGGCCCAAGATGCAAAGTGTGCCGGAGCTGGCCAA  
SEQID1 CGGCGACCTCAAGGACGCCCCATGGTGGCCCAAGATGCAAAGTGTGCCGGAGCTGGCCAA  
SEQID2 CGGCGACCTCAAGGACGCCCCATGGTGGCCCAAGATGCAAAGTGTGCCGGAGCTGGCCAA  
\*\*\*\*\*

SEQID5 GGCGTGACCAACCATCATCTGGATCGGGTCGGCGCTGCATGCGGCAGTCAACTTCGGGCA  
SEQID6 GGCGTGACCAACCATCATCTGGATCGGGTCGGCGCTGCATGCGGCAGTCAACTTCGGGCA  
SEQID1 GGCGTGACCAACCATCATCTGGATCGGGTCGGCGCTGCATGCGGCAGTCAACTTCGGGCA  
SEQID2 GGCGTGACCAACCATCATCTGGATCGGGTCGGCGCTGCATGCGGCAGTCAACTTCGGGCA  
\*\*\*\*\*

SEQID5 GTACCCCTACGCGGGGTTCTCCCGAACCGGCCGACGGTGAGCCGGCGCCGCATGCCGGA  
SEQID6 GTACCCCTACGCGGGGTTCTCCCGAACCGGCCGACGGTGAGCCGGCGCCGCATGCCGGA  
SEQID1 GTACCCCTACGCGGGGTTCTCCCGAACCGGCCGACGGTGAGCCGGCGCCGCATGCCGGA  
SEQID2 GTACCCCTACGCGGGGTTCTCCCGAACCGGCCGACGGTGAGCCGGCGCCGCATGCCGGA  
\*\*\*\*\*



SEQID5	GCCCCGGCACGGAGGAGTACGCGGAGCTGGAGCGCGACCCGGAGCGGGCCTTCATCCACAC
SEQID6	GCCCCGGCACGGAGGAGTACGCGGAGCTGGAGCGCGACCCGGAGCGGGCCTTCATCCACAC
SEQID1	GCCCCGGCACGGAGGAGTACGCGGAGCTGGAGCGCGACCCGGAGCGGGCCTTCATCCACAC
SEQID2	GCCCCGGCACGGAGGAGTACGCGGAGCTGGAGCGCGACCCGGAGCGGGCCTTCATCCACAC
	*****
SEQID5	CATCACGAGCCAGATCCAGACCATCATCGGCGTGTCGCTGCTGGAGGTGCTGTCGAAGCA
SEQID6	CATCACGAGCCAGATCCAGACCATCATCGGCGTGTCGCTGCTGGAGGTGCTGTCGAAGCA
SEQID1	CATCACGAGCCAGATCCAGACCATCATCGGCGTGTCGCTGCTGGAGGTGCTGTCGAAGCA
SEQID2	CATCACGAGCCAGATCCAGACCATCATCGGCGTGTCGCTGCTGGAGGTGCTGTCGAAGCA
	*****
SEQID5	CTCCTCCGACGAGCTGTACCTCGGGCAGCGGGACACGCCGGAGTGACCTCGGACCCAAA
SEQID6	CTCCTCCGACGAGCTGTACCTCGGGCAGCGGGACACGCCGGAGTGACCTCGGACCCAAA
SEQID1	CTCCTCCGACGAGCTGTACCTCGGGCAGCGGGACACGCCGGAGTGACCTCGGACCCAAA
SEQID2	CTCCTCCGACGAGCTGTACCTCGGGCAGCGGGACACGCCGGAGTGACCTCGGACCCAAA
	*****
SEQID5	GGCCCTGGAGGTGTTCAAGCGGTTTCAGCGACCGGCTGGTGGAGATCGAGAGCAAGGTGGT
SEQID6	GGCCCTGGAGGTGTTCAAGCGGTTTCAGCGACCGGCTGGTGGAGATCGAGAGCAAGGTGGT
SEQID1	GGCCCTGGAGGTGTTCAAGCGGTTTCAGCGACCGGCTGGTGGAGATCGAGAGCAAGGTGGT
SEQID2	GGCCCTGGAGGTGTTCAAGCGGTTTCAGCGACCGGCTGGTGGAGATCGAGAGCAAGGTGGT
	*****
SEQID5	GGGCATGAACCATGACCCGGAGCTCAAGAACCGCAACGGCCCCGGCTAAGTTTCCCTACAT
SEQID6	GGGCATGAACCATGACCCGGAGCTCAAGAACCGCAACGGCCCCGGCTAAGTTTCCCTACAT
SEQID1	GGGCATGAACCATGACCCGGAGCTCAAGAACCGCAACGGCCCCGGCTAAGTTTCCCTACAT
SEQID2	GGGCATGAACCATGACCCGGAGCTCAAGAACCGCAACGGCCCCGGCTAAGTTTCCCTACAT
	*****
SEQID5	GCTGCTCTACCCCAACACCTCCGACCACAAGGGCGCCGCTGCCGGGCTTACCGCCAAGGG
SEQID6	GCTGCTCTACCCCAACACCTCCGACCACAAGGGCGCCGCTGCCGGGCTTACCGCCAAGGG
SEQID1	GCTGCTCTACCCCAACACCTCCGACCACAAGGGCGCCGCTGCCGGGCTTACCGCCAAGGG
SEQID2	GCTGCTCTACCCCAACACCTCCGACCACAAGGGCGCCGCTGCCGGGCTTACCGCCAAGGG
	*****
SEQID5	CATCCCCAACAGCATCTCCATCTAA
SEQID6	CATCCCCAACAGCATCTCCATCTAA
SEQID1	CATCCCCAACAGCATCTCCATCTAA
SEQID2	CATCCCCAACAGCATCTCCATCTAA
	*****

# LOX-1 Protein

# Compare WT/MUTANTS

CLUSTAL W (1.8) multiple sequence alignment

ClBarke cv. Neruda	SEQID3	WT	MLLGGLIDTLTGANKSARLKGTVVLMRKNVLDLNDFGATIIDGIGEFGLGKGVTCQLISST	60
	SEQID4	MUTD112	MLLGGLIDTLTGANKSARLKGTVVLMRKNVLDLNDFGATIIDGIGEFGLGKGVTCQLISST	
	SEQID7	WT	MLLGGLIDTLTGANKSARLKGTVVLMRKNVLDLNDFGATIIDGIGEFGLGKGVTCQLISST	
	SEQID8	MUT A618	MLLGGLIDTLTGANKSARLKGTVVLMRKNVLDLNDFGATIIDGIGEFGLGKGVTCQLISST *****	
	SEQID3		AVDQDNGGRGKVGAEAELEQWVTSLSPLTTGESKFGLTFDWEVEKLGVPGAIVVNNYHSS	120
	SEQID4		AVDQDNGGRGKVGAEAELEQWVTSLSPLTTGESKFGLTFDWEVEKLGVPGAIVVNNYHSS	
	SEQID7		AVDQDNGGRGKVGAEAELEQWVTSLSPLTTGESKFGLTFDWEVEKLGVPGAIVVNNYHSS	
	SEQID8		AVDQDNGGRGKVGAEAELEQWVTSLSPLTTGESKFGLTFDWEVEKLGVPGAIVVNNYHSS *****	
	SEQID3		EFLCLKTITLHDPVGRSGNLTTFVANSWIYPAANYRYSRVFFANDTYLPSQMPAALKPYRDD	180
	SEQID4		EFLCLKTITLHDPVGRSGNLTTFVANSWIYPAANYRYSRVFFANDTYLPSQMPAALKPYRDD	
	SEQID7		EFLCLKTITLHDPVGRSGNLTTFVANSWIYPAANYRYSRVFFANDTYLPSQMPAALKPYRDD	
	SEQID8		EFLCLKTITLHDPVGRSGNLTTFVANSWIYPAANYRYSRVFFANDTYLPSQMPAALKPYRDD *****	
	SEQID3		ELRNLRGDDQQGPYQEHDRYRYDVYNDLGEGRPILGGNSDHPYPRRGRTERKPNASDPS	240
	SEQID4		ELRNLRGDDQQGPYQEHDRYRYDVYNDLGEGRPILGGNSDHPYPRRGRTERKPNASDPS	
	SEQID7		ELRNLRGDDQQGPYQEHDRYRYDVYNDLGEGRPILGGNSDHPYPRRGRTERKPNASDPS	
	SEQID8		ELRNLRGDDQQGPYQEHDRYRYDVYNDLGEGRPILGGNSDHPYPRRGRTERKPNASDPS *****	
	SEQID3		LESRLSLLEQIYVPRDEKFGHLKTSDFLGYSIKAITQGILPAVRTYVDTTPEGFDSFQDI	300
	SEQID4		LESRLSLLEQIYVPRDEKFGHLKTSDFLGYSIKAITQGILPAVRTYVDTTPEGFDSFQDI	
	SEQID7		LESRLSLLEQIYVPRDEKFGHLKTSDFLGYSIKAITQGILPAVRTYVDTTPEGFDSFQDI	
	SEQID8		LESRLSLLEQIYVPRDEKFGHLKTSDFLGYSIKAITQGILPAVRTYVDTTPEGFDSFQDI *****	
	SEQID3		INLYEGGIKLPKVAALEELRKQFPLQLIKDLLPVGGDSLLKLPVPHIIQENKQAWRTDEE	360
	SEQID4		INLYEGGIKLPKVAALEELRKQFPLQLIKDLLPVGGDSLLKLPVPHIIQENKQAWRTDEE	
	SEQID7		INLYEGGIKLPKVAALEELRKQFPLQLIKDLLPVGGDSLLKLPVPHIIQENKQAWRTDEE	
	SEQID8		INLYEGGIKLPKVAALEELRKQFPLQLIKDLLPVGGDSLLKLPVPHIIQENKQAWRTDEE *****	
	SEQID3		FAREVLAVGNPVMITRLTEFPPKSSLDPSKFGDHTSTITAHEIEKNLEGLTVQQALESNR	420
	SEQID4		FAREVLAVGNPVMITRLTEFPPKSSLDPSKFGDHTSTITAHEIEKNLEGLTVQQALESNR	
	SEQID7		FAREVLAVGNPVMITRLTEFPPKSSLDPSKFGDHTSTITAHEIEKNLEGLTVQQALESNR	
	SEQID8	A618	FAREVLAVGNPVMITR-----L-----IMS----- ***** 376  377      378	
	SEQID3		LYILDHHDRFMPFLIDVNNLPGNFIYATRTLFFLRGDGRLTPLAIELSEPIIQGGLTTAK	480
	SEQID4		LYILDHHDRFMPFLIDVNNLPGNFIYATRTLFFLRGDGRLTPLAIELSEPIIQGGLTTAK	
	SEQID7		LYILDHHDRFMPFLIDVNNLPGNFIYATRTLFFLRGDGRLTPLAIELSEPIIQGGLTTAK	
	SEQID8		-----QRL--FVHCVCVMVS--MVRKCRS----- *:  *:  *  .:  .:  *:	
	SEQID3		SKVYTPVPSGSVEGWVWELAKAYVAVNDSGWHQLVSHWLNTHAVMEPFVISTNRHLSVTH	540
	SEQID4		SKVYTPVPSGSVEGWVWELAKAYVAVNDSGWHQLVSHWLNTHAVMEPFVISTNRHLSVTH	
	SEQID7		SKVYTPVPSGSVEGWVWELAKAYVAVNDSGWHQLVSHWLNTHAVMEPFVISTNRHLSVTH	
	SEQID8		-----	

Mutant A618 = splice Variant / truncation of LOX-1  
at 378 (3)

SEQID3 PVHKLLSPHYRDTMTINALARQTLINAGGIFEMTVFPGKFALGMSAVVYKDWKFTEQGLP 600  
 SEQID4 PVHKLLSPHYRDTMTINALARQTLINAGGIFEMTVFPGKFALGMSAVVYKDWKFTEQGLP  
 SEQID7 PVHKLLSPHYRDTMTINALARQTLINAGGIFEMTVFPGKFALGMSAVVYKDWKFTEQGLP  
 SEQID8 -----

SEQID3 DDLIKRGMAVEDPSSPYKVRLLVSDYPYAADGLAIWHAIEQYVSEYLAIYYPNDGVLQGD 660  
 SEQID4 DDLIKRGMAVEDPSSPYKVRLLVSDYPYAADGLAIWHAIEQYVSEYLAIYYPNDGVLQGD  
 SEQID7 DDLIKRGMAVEDPSSPYKVRLLVSDYPYAADGLAIWHAIEQYVSEYLAIYYPNDGVLQGD  
 SEQID8 -----

SEQID3 TEVQAWWKETREVGHGDLKDAPWWPKMQSVPELAKACTTIIWIGSALHAAVNFGQYPYAG 720  
 SEQID4 TEVQA-----  
 SEQID7 TEVQAWWKETREVGHGDLKDAPWWPKMQSVPELAKACTTIIWIGSALHAAVNFGQYPYAG  
 SEQID8 -----

SEQID3 FLPNRPTVSRRRMPEPGTEEYAELEERDPERAFIHTTITSQIQTIIGVSLLEVL SKHSSDEL 780  
 SEQID4 -----  
 SEQID7 FLPNRPTVSRRRMPEPGTEEYAELEERDPERAFIHTTITSQIQTIIGVSLLEVL SKHSSDEL  
 SEQID8 -----

SEQID3 YLGQRDTPewTSDPKALEVFKRFSdRLVEIESKVVGmNHDPELKNRNGPAKFPYmLLYPN 840  
 SEQID4 -----  
 SEQID7 YLGQRDTPewTSDPKALEVFKRFSdRLVEIESKVVGmNHDPELKNRNGPAKFPYmLLYPN  
 SEQID8 -----

862  
 SEQID3 TSDHKGAAAGLTAKGIPNSISI  
 SEQID4 -----  
 SEQID7 TSDHKGAAAGLTAKGIPNSISI  
 SEQID8 -----

Mutant D112 - truncated at 665

